1812

> **This Raw Listing contains the General
> Information Section and up to the first 5 pages.**

```
 1                                    SEQUENCE LISTING        ENTERED
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: GREENE, JOHN M
 6                       FLEISCHMANN, ROBERT D
 7
 8       (ii) TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR
 9
10      (iii) NUMBER OF SEQUENCES: 10
11
12       (iv) CORRESPONDENCE ADDRESS:
13            (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
14            (B) STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
15            (C) CITY: WASHINGTON
16            (D) STATE: DC
17            (E) COUNTRY: US
18            (F) ZIP: 20005-3934
19
20        (v) COMPUTER READABLE FORM:
21            (A) MEDIUM TYPE: Floppy disk
22            (B) COMPUTER: IBM PC compatible
23            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26       (vi) CURRENT APPLICATION DATA:
27            (A) APPLICATION NUMBER: US 08/469,637
28            (B) FILING DATE: 06-JUN-1995
29            (C) CLASSIFICATION:
30
31    (viii) ATTORNEY/AGENT INFORMATION:
32            (A) NAME: STEFFE, ERIC K
33            (B) REGISTRATION NUMBER: 36,688
34            (C) REFERENCE/DOCKET NUMBER: 1488.0710001
35
36       (ix) TELECOMMUNICATION INFORMATION:
37            (A) TELEPHONE: (202) 371-2600
38            (B) TELEFAX: (202) 371 2540
39
40
41    (2) INFORMATION FOR SEQ ID NO:1:
42
43        (i) SEQUENCE CHARACTERISTICS:
44            (A) LENGTH: 1527 base pairs
45            (B) TYPE: nucleic acid
46            (C) STRANDEDNESS: double
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/469,637A*

INPUT SET: S19007.raw

```
47                    (D) TOPOLOGY: linear
48
49        (ii) MOLECULE TYPE: DNA (genomic)
50
51
52        (ix) FEATURE:
53              (A) NAME/KEY: CDS
54              (B) LOCATION: 46..1248
55
56        (ix) FEATURE:
57              (A) NAME/KEY: sig_peptide
58              (B) LOCATION: 46..106
59
60        (ix) FEATURE:
61              (A) NAME/KEY: mat_peptide
62              (B) LOCATION: 109..1248
63
64
65        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67  CGCCCAGCCG CCGCCTCCAA GCCCCTGAGG TTTCCGGGGA CCACA ATG AAC AAG          54
68                                                      Met Asn Lys
69                                                      -21 -20
70
71  TTG CTG TGC TGC GCG CTC GTG TTT CTG GAC ATC TCC ATT AAG TGG ACC        102
72  Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr
73          -15                 -10                     -5
74
75  ACC CAG GAA ACG TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC        150
76  Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr
77          1               5                   10
78
79  TCT CAT CAG CTG TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA        198
80  Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys
81   15                 20                  25                  30
82
83  CAA CAC TGT ACA GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC        246
84  Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp
85                  35                  40                  45
86
87  CAC TAC TAC ACA GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC        294
88  His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys
89                  50                  55                  60
90
91  AGC CCC GTG TGC AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC        342
92  Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg
93          65                  70                  75
94
95  ACC CAC AAC CGC GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA        390
96  Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile
97      80                  85                  90
98
99  GAG TTC TGC TTG AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG        438
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INPUT SET: S19007.raw

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100   Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val
101    95              100             105             110
102

103   CAA GCT GGA ACC CCA GAG CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT        486
104   Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp
105                 115             120             125

106

107   GGG TTC TTC TCA AAT GAG ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC        534
108   Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His
109                 130             135             140

110

111   ACA AAT TGC AGT GTC TTT GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA        582
112   Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala
113             145             150             155

114

115   ACA CAC GAC AAC ATA TGT TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT        630
116   Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
117         160             165             170

118

119   GGA ATA GAT GTT ACC CTG TGT GAG GAG GCA TTC TTC AGG TTT GCT GTT        678
120   Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val
121   175             180             185             190

122

123   CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT GTC TTG GTA GAC AAT TTG        726
124   Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu
125                 195             200             205

126

127   CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA GAG AGG ATA AAA CGG CAA        774
128   Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln
129                 210             215             220

130

131   CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG CTG AAG TTA TGG AAA CAT        822
132   His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His
133             225             230             235

134

135   CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG ATC ATC CAA GAT ATT GAC        870
136   Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp
137         240             245             250

138

139   CTC TGT GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT AAC CTC ACC        918
140   Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr
141   255             260             265             270

142

143   TTC GAG CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA AAG AAA GTG        966
144   Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val
145                 275             280             285

146

147   GGA GCA GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA CCC AGT GAC       1014
148   Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp
149                 290             295             300

150

151   CAG ATC CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT GGC GAC CAA       1062
152   Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln
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INPUT SET: S19007.raw

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153              305                    310                    315
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155    GAC ACC TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA AAG ACG TAC      1110
156    Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr
157        320                    325                    330
158
159    CAC TTT CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC ATC AGG TTC      1158
160    His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe
161    335                    340                    345                    350
162
163    CTT CAC AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA TTT TTA GAA      1206
164    Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu
165                    355                    360                    365
166
167    ATG ATA GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA              1248
168    Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
169                    370                    375                    380
170
171    TAACTGGAAA TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGAGTAA      1308
172
173    ACTGTTTCTC AGGCACTTGA GGCTTTCAGT GATATCTTTC TCATTACCAG TGACTAATTT      1368
174
175    TGCCACAGGG TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT CCTCCAATAA      1428
176
177    ACCCCAAATG GTTAATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT ATATTTTCCC      1488
178
179    TTATTACTGC TTGCAGTAAT TCAACTGGAA AAAAAAAAA                            1527
180
181
182    (2) INFORMATION FOR SEQ ID NO:2:
183
184         (i) SEQUENCE CHARACTERISTICS:
185              (A) LENGTH: 401 amino acids
186              (B) TYPE: amino acid
187              (D) TOPOLOGY: linear
188
189         (ii) MOLECULE TYPE: protein
190
191         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
192
193    Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
194    -21 -20                 -15                 -10
195
196    Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
197     -5                 1             5                   10
198
199    Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
200              15                 20                   25
201
202    Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
203         30                 35                   40
204
205    Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
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INPUT SET: S19007.raw

```
206            45                        50                        55
207
208    Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
209     60              65                  70                      75
210
211    Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
212                 80                  85                  90
213
214    Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
215                 95                 100                 105
216
217    Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
218             110             115                 120
219
220    Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
221        125             130                 135
222
223    Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
224    140                 145                 150                     155
225
226    Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
227                 160                 165                 170
228
229    Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
230             175                 180                 185
231
232    Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
233             190                 195                 200
234
235    Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
236        205                 210                 215
237
238    Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
239    220                 225                 230                     235
240
241    Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
242                 240                 245                 250
243
244    Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
245             255                 260                 265
246
247    Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
248             270                 275                 280
249
250    Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
251        285                 290                 295
252                                      •
253    Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
254    300             305                 310                     315
255
256    Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
257             320                 325                 330
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/469,637A*

INPUT SET: S19007.raw

Line	Error	Original Text